

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> Method of screening modified antibody having agonistic activity

<130> C1-A0322P

<150> JP 2003-415733

<151> 2003-12-12

<160> 15

<170> PatentIn version 3.1

<210> 1

<211> 21

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

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gggccagtgg atagacagat g

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gctcaactgga tggtgccaag atg

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<222> (1)..(411)  
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 Met Glu Trp Pro Leu Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly  
 1 5 10 15

gtc cac tcc cag gtt cag ctg cag cag tct gga cct gag ttg gtg aag 96  
 Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys  
 20 25 30

cct ggg gcc tca gtg aag att tcc tgc aag gct tct ggc tat gca ttc 144  
 Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe  
 35 40 45

agt agt tcc tgg atg aac tgg gtg aag cag agg cct gga aag ggt ctt 192  
 Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu  
 50 55 60

gag tgg att gga cg<sup>g</sup> att tat cct gga gat gga gat act aac tac aat 240  
 Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn  
 65 70 75 80

ggg aag ttc aag ggc aag gcc aca ctg act gca gac aaa tcc tcc agc 288  
 Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser  
 85 90 95

acg gcc tac ata caa ctc agc agc cta aca tct gag gac tct gcg gtc 336  
 Thr Ala Tyr Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val  
                   100                  105                  110

tac ttc tgt gca aga ggg tat gct gac tac tcc ttt gct tac tgg ggc 384  
 Tyr Phe Cys Ala Arg Gly Tyr Ala Asp Tyr Ser Phe Ala Tyr Trp Gly  
 115 120 125

caa ggg act ctg gtc act gtc tct gca 411  
Gln Gly Thr Leu Val Thr Val Ser Ala  
130 135

<210> 4

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<212> PRT

<213> *Mus musculus*

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Met Glu Trp Pro Leu Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly  
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Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys  
20 25 30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe  
35 40 45

Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn  
 65 70 75 80

Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser  
 85 90 95

Thr Ala Tyr Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val  
 100 105 110

Tyr Phe Cys Ala Arg Gly Tyr Ala Asp Tyr Ser Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ala  
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<212> DNA

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 Met Arg Cys Leu Ala Glu Phe Leu Gly Leu Leu Val Leu Trp Ile Pro  
 1 5 10 15

gga gcc att ggg gat att gtg atg act cag gct gca ccc tct gta cct 96  
 Gly Ala Ile Gly Asp Ile Val Met Thr Gln Ala Ala Pro Ser Val Pro  
 20 25 30

gtc act cct gga gag tca gta tcc atc tcc tgc agg tct agt aag agt 144  
 Val Thr Pro Gly Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser  
 35 40 45

ctc ctg cat agt aat ggc aac act tac ttg tat tgg ttc ctg cag agg 192  
 Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg  
 50 55 60

cca ggc cag tct cct cag ctc ctg ata tat cgg atg tcc aac ctt gcc	240		
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala			
65	70	75	80
tca gga gtc cca gac agg ttc agt ggc agt ggg tca gga act gct ttc	288		
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Ala Phe			
85	90	95	
aca ctg aga atc agt aga gtg gag gct gag gat gtg ggt gtt tat tac	336		
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr			
100	105	110	
tgt atg caa cat cta gaa tat ccg tat acg ttc gga tcg ggg acc aag	384		
Cys Met Gln His Leu Glu Tyr Pro Tyr Thr Phe Gly Ser Gly Thr Lys			
115	120	125	
ctg gaa ata aaa	396		
Leu Glu Ile Lys			
130			
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Met Arg Cys Leu Ala Glu Phe Leu Gly Leu Leu Val Leu Trp Ile Pro			
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Gly Ala Ile Gly Asp Ile Val Met Thr Gln Ala Ala Pro Ser Val Pro			
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Val Thr Pro Gly Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser			
35	40	45	
Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg			

50

55

60

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala  
 65 70 75 80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe  
 85 90 95

Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr  
 100 105 110

Cys Met Gln His Leu Glu Tyr Pro Tyr Thr Phe Gly Ser Gly Thr Lys  
 115 120 125

Leu Glu Ile Lys  
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<210> 7

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<212> DNA

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tagaattcca ccatggaatg gcctttgatc

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agcctgagtc atcacaatat ccgatccgcc tccacacctgca gagacagtga ccagag 56

<210> 9

<211> 56

<212> DNA

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<223> an artificially synthesized primer sequence

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actctggtca ctgtctctgc aggtggaggc ggatcggata ttgtgatgac tcaggc 56

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<211> 60

<212> DNA

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attgcggccg cttatcactt atcgtcgtca tcctttagt cttttatttc cagcttggtc 60

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<211> 8

<212> PRT

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Asp Tyr Lys Asp Asp Asp Asp Lys

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<212> DNA

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<400> 12

tgagtcatca caatatccga tccgccacca cccgaaccac caccacccga accaccacca 60

cctgcagaga cagtgaccag ag 82

<210> 13

<211> 82

<212> DNA

<213> Artificial

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<223> an artificially synthesized primer sequence

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tggtcactgt ctctgcaggt ggtgggggtt cgggtgggtgg tggttcgggt ggtggcggat 60

cggatattgt gatgactcag gc 82

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<212> DNA

<213> Artificial

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<400> 14

caggttcagc tgcagcagtc tggac 25

<210> 15

<211> 81

<212> DNA

<213> Artificial

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<223> an artificially synthesized primer sequence

<400> 15

gctgcagctg aacctgcgat ccaccgcctc ccgaaccacc accaccgat ccaccacctc 60

cttttatttc cagcttggtc c 81